SEQUENCE LISTING

<110> Bristol-Myers Squibb Company

<120> POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL BETA-SUBUNIT, K+betaM2

<130> D0076 NP <150> US 60/263,872 <151> 2001-01-24 <150> US 60/269,794 <151> 2001-02-14 <160> 73 <170> PatentIn version 3.0 <210> 1 <211> 3468 <212> DNA <213> Homo sapiens <220> CDS <221> (515)..(1798) <222> <400> 1 60 caaqcactqt qctaaaqtqt ttttcatatq tcatgaaaag ttgtgccaga aaattatggt ttgaacatgg gcagttttct cctaccgtca gctatatcca caagcatcac atgaagtgga 120 180 gatctggcag ctctgtgtat ttcagtcaag ttccacaatg aaacctgaca ataatggtaa aaaccaatac ggacatctga gtaactgggg aattggcctg ccttgcatgt gagcttgatg 240 gaagattgga tatagacgag ttgattatat tttatgaagt agcagctcac taccatccac 300 360 catccagggt ttaaactact ttttcagcat cacttcacct gtggactctt atacattttg 420 atttcttqqq qqaaaaatac tqqqataaqa qqaqqtcatt ttttaataaq ttaqcatcct tttccctttc ttacaaqttq atccaaagga taaggctgtg actccattgg attgcacctt 480 535 taaatcaaaa tagcagcagc agaagaaagg gaca atg gct ctg agt gga aac tgt Met Ala Leu Ser Gly Asn Cys agt cgt tat tat cct cga gaa caa ggg tcc gca gtt ccc aac tcc ttc 583 Ser Arg Tyr Tyr Pro Arg Glu Gln Gly Ser Ala Val Pro Asn Ser Phe 631 cct qaq qtq qta gag ctg aat gtc ggg ggt caa gtt tat ttt act cgc Pro Glu Val Val Glu Leu Asn Val Gly Gly Gln Val Tyr Phe Thr Arg

35

30

cat His 40	tcc Ser	aca Thr	ttg Leu	ata Ile	agc Ser 45	atc Ile	cct Pro	cat His	tcc Ser	ctc Leu 50	ctg Leu	tgg Trp	aaa Lys	atg Met	ttt Phe 55	679)
tcc Ser	cca Pro	aag Lys	aga Arg	gac Asp 60	acg Thr	gct Ala	aat Asn	gat Asp	cta Leu 65	gcc Ala	aag Lys	gac Asp	tcc Ser	aag Lys 70	gga Gly	727	7
agg Arg	ttt Phe	ttc Phe	att Ile 75	gac Asp	aga Arg	gat Asp	gga Gly	ttc Phe 80	ttg Leu	ttc Phe	cgt Arg	tat Tyr	att Ile 85	ctg Leu	gac Asp	775	5
tat Tyr	ctc Leu	agg Arg 90	gac Asp	agg Arg	cag Gln	gtg Val	gtc Val 95	ctg Leu	cct Pro	gat Asp	cac His	ttt Phe 100	cca Pro	gaa Glu	aaa Lys	823	3
gga Gly	aga Arg 105	ctg Leu	aaa Lys	agg Arg	gaa Glu	gct Ala 110	gaa Glu	tac Tyr	ttc Phe	cag Gln	ctc Leu 115	cca Pro	gac Asp	ttg Leu	gtc Val	871	1
aaa Lys 120	ctc Leu	ctg Leu	acc Thr	ccc Pro	gat Asp 125	gaa Glu	atc Ile	aag Lys	caa Gln	agc Ser 130	cca Pro	gat Asp	gaa Glu	ttc Phe	tgc Cys 135	91:	9
cac His	agt Ser	gac Asp	ttt Phe	gaa Glu 140	gat Asp	gcc Ala	tcc Ser	caa Gln	gga Gly 145	agc Ser	gac Asp	aca Thr	aga Arg	atc Ile 150	tgc Cys	96	7
ccc Pro	cct Pro	tcc Ser	tcc Ser 155	ctg Leu	ctc Leu	cct Pro	gcc Ala	gac Asp 160	cgc Arg	aag Lys	tgg Trp	ggt Gly	ttc Phe 165	att Ile	act Thr	101	5
gtg Val	ggt Gly	tac Tyr 170	aga Arg	gga Gly	tcc Ser	tgc Cys	acc Thr 175	ttg Leu	ggc Gly	aga Arg	gag Glu	gga Gly 180	cag Gln	gca Ala	gat Asp	106	3
gcc Ala	aag Lys 185	ttt Phe	cgg Arg	aga Arg	gtt Val	ccc Pro 190	cgg Arg	att Ile	ttg Leu	gtt Val	tgt Cys 195	gga Gly	agg Arg	att Ile	tcc Ser	111	1
ttg Leu 200	gca Ala	aaa Lys	gaa Glu	gtc Val	ttt Phe 205	gga Gly	gaa Glu	act Thr	ttg Leu	aat Asn 210	gaa Glu	agc Ser	aga Arg	gac Asp	cct Pro 215	115	9
gat Asp	cga Arg	gcc Ala	cca Pro	gaa Glu 220	aga Arg	tac Tyr	acc Thr	tcc Ser	aga Arg 225	ttt Phe	tat Tyr	ctc Leu	aaa Lys	ttc Phe 230		120	7
cac His	ctg Leu	gaa Glu	agg Arg 235	gct Ala	ttt Phe	gat Asp	atg Met	ttg Leu 240	tca Ser	gag Glu	tgt Cys	gga Gly	ttc Phe 245	His	atg Met	125	5
gtg Val	gcc Ala	tgt Cys 250	Asn	tca Ser	tcg Ser	gtg Val	aca Thr 255	Ala	tct Ser	ttc Phe	atc Ile	aac Asn 260	Gln	tat Tyr	aca Thr	130	3
gat	gac	aag	atc	tgg	tca	agc	tac	act	gaa	tat	gtc	ttc	tac	: cgt	gag	135	1

Asp	Asp 265	Lys	Ile	Trp	Ser	Ser 270	Tyr	Thr	Glu	Tyr	Val 275	Phe	Tyr	Arg	Glu	
cct Pro 280	tcc Ser	aga Arg	tgg Trp	tca Ser	ccc Pro 285	tca Ser	cac His	tgc Cys	gat Asp	tgc Cys 290	tgc Cys	tgc Cys	aag Lys	aat Asn	ggc Gly 295	1399
aaa Lys	ggt Gly	gac Asp	aaa Lys	gaa Glu 300	ggg ggg	gag Glu	agc Ser	ggc Gly	acg Thr 305	tct Ser	tgc Cys	aat Asn	gac Asp	ctc Leu 310	tcc Ser	1447
aca Thr	tct Ser	agc Ser	tgc Cys 315	gac Asp	agc Ser	cag Gln	tct Ser	gag Glu 320	gcc Ala	agc Ser	tct Ser	ccc Pro	cag Gln 325	gag Glu	acg Thr	1495
gtc Val	atc Ile	tgt Cys 330	ggt Gly	ccc Pro	gtg Val	aca Thr	cgc Arg 335	cag Gln	acc Thr	aac Asn	atc Ile	cag Gln 340	act Thr	ctg Leu	gac Asp	1543
cgt Arg	ccc Pro 345	atc Ile	aag Lys	aag Lys	ggc Gly	cct Pro 350	gtc Val	cag Gln	ctg Leu	atc Ile	caa Gln 355	cag Gln	tca Ser	gag Glu	atg Met	1591
cgg Arg 360	cgg Arg	aaa Lys	agc Ser	gac Asp	tta Leu 365	ctc Leu	cgg Arg	att Ile	ctg Leu	act Thr 370	tca Ser	ggc Gly	tcc Ser	agg Arg	gaa Glu 375	1639
tcg Ser	aac Asn	atg Met	agc Ser	agc Ser 380	aaa Lys	aaa Lys	aaa Lys	gct Ala	gtt Val 385	aaa Lys	gaa Glu	aag Lys	ctc Leu	tca Ser 390	att Ile	1687
gag Glu	gag Glu	gag Glu	ctg Leu 395	gag Glu	aaa Lys	tgt Cys	atc Ile	cag Gln 400	gat Asp	ttc Phe	cta Leu	aaa Lys	aaa Lys 405	aaa Lys	att Ile	1735
cca Pro	gat Asp	cgg Arg 410	ttt Phe	cct Pro	gag Glu	aga Arg	aaa Lys 415	cat His	cct Pro	tgg Trp	caa Gln	tct Ser 420	gaa Glu	ctt Leu	tta Leu	1783
Arg		tat Tyr			taa	ggga	ggg	ctgg	gggc	gg g	gaaa	aaaa	a aa	aaaa	gagt	1838
cat	tttg	aaa '	ttaa	cctc	at a	aaag	gaat	t ca	tatt	ttaa	agg	aaaa	aaa	taca	actaat	1898
gat	gcac	att ·	tctt	agaa	ca c	aata	gtcc	a tt	gata	tact	act	gcct	act	ttac	ctagtt	1958
cac	ctta	aca ·	tgta	aatc	ca c	aggg	taga	t tt	cttt	ctag	atg	tgga	agt	acaa	gaaaat	2018
ctt	tttt	agt	tatt	tgtt	tg t	ttac	ttcg	t cc	catg	tgct	aac	tatc	tta	tata	taatga	2078
gag	ccag	cta	cgta	aaag	ta g	ctga	gagg	c ct	tggg	agtc	att	tatc	cca	aact	gggttt	2138
ttt	ctct	cat	cctt	ctac	ct c	cctc	cttt	g aa	tgag	ggta	tgg	taga	aaa	agat	ctggcc	2198
caa	tggc	ata	agtt	tgga	at t	ttta	attt	t gg	tttt	tcct	ttt	gttt	atg	gggt	tggggg	2258

gaatggcaga	tttatatgac	ttttcactca	aatctatatg	tgccagttta	tattgactcc	2318
gtatgcatga	gtatttgtgc	aacacaagca	caactaagta	tgtatataca	catgacgcac	2378
acgatgccag	ggcctagacc	tcccaagggc	tgtgctcctg	ctcccagcag	ccctctctta	2438
gaatatttca	gatggatgag	cttctgactc	tttcttaaaa	ttcttttggg	aagatttccc	2498
agcctttctt	cacaacactt	tctaacatca	aatgactctc	atcatcaaca	aattgtattc	2558
cttattgtga	aattaatacc	ctcaggctcc	attttactgc	tttgctcttt	gtctgcatta	2618
agagaggatg	aggagagctg	gtcaaacatt	ccttgtgtta	aaaaaatcaa	acattcatat	2678
ccacaaaatt	ttctgctaaa	tgactccaca	ctcagecttc	tctaccctga	actgaattat	2738
cacccttttc	tccatgtttt	cagagttctt	actgcccaca	gtttaatggt	gtggcctttc	2798
cacataatcc	acattaagtt	ctgtgttcct	gtgttgttgt	ggaactaagg	acaacacaca	2858
gtacttgaat	aagggtccgg	ccttttgttt	gttttagaga	aagttgtatt	ccacacacaa	2918
cctaataatt	tcttataaaa	attttaaact	acaaagctac	atttttactt	gcttgtagcc	2978
gtttttgttt	gcctttggga	ttcgggcttt	ggctgtgccc	atgctaggat	ttagctgtgt	3038
catttttatg	atgtctgtaa	caacccaaca	aggtaactga	agctccagag	ttaaggtttc	3098
agatttctaa	atgaaactat	ctttttcaat	tacatcctga	cttgtataga	cacagccaaa	3158
aagaaactgt	taatagccat	ccgtccatgt	aactctgtat	tttactaagg	taccaatagc	3218
tctttcatag	acttgtgcta	caagaaggtt	aaaagaccag	ttttattttc	agcattcctc	3278
atgcatttca	gtggtaacca	aaaaataatt	tgtcaattaa	tagttgtgtg	ccaagcactc	3338
ctaatttgtt	ttattgcgtg	tgtgtgcatg	tgtgtatgtg	tatcacaggt	aataaaggca	3398
attggatgat	taaaaaaaaa	aaaaaaaaa	aaaaaaaaa	aaaaaaaaa	aaaaaaaaaa	3458
aaaaaaaaa						3468

<210> 2

Met Ala Leu Ser Gly Asn Cys Ser Arg Tyr Tyr Pro Arg Glu Gln Gly 1 5 10 15

Ser Ala Val Pro Asn Ser Phe Pro Glu Val Val Glu Leu Asn Val Gly 20 25 30

<211> 428

<212> PRT

<213> Homo sapiens

<400> 2

Gly Gln Val Tyr Phe Thr Arg His Ser Thr Leu Ile Ser Ile Pro His 35 40 45

Ser Leu Leu Trp Lys Met Phe Ser Pro Lys Arg Asp Thr Ala Asn Asp 50 55 60

Leu Ala Lys Asp Ser Lys Gly Arg Phe Phe Ile Asp Arg Asp Gly Phe 65 70 75 80

Leu Phe Arg Tyr Ile Leu Asp Tyr Leu Arg Asp Arg Gln Val Val Leu 85 90 95

Pro Asp His Phe Pro Glu Lys Gly Arg Leu Lys Arg Glu Ala Glu Tyr 100 105 110

Phe Gln Leu Pro Asp Leu Val Lys Leu Leu Thr Pro Asp Glu Ile Lys 115 120 125

Gln Ser Pro Asp Glu Phe Cys His Ser Asp Phe Glu Asp Ala Ser Gln 130 135 140

Gly Ser Asp Thr Arg Ile Cys Pro Pro Ser Ser Leu Leu Pro Ala Asp 145 150 155 160

Arg Lys Trp Gly Phe Ile Thr Val Gly Tyr Arg Gly Ser Cys Thr Leu 165 170 175

Gly Arg Glu Gly Gln Ala Asp Ala Lys Phe Arg Arg Val Pro Arg Ile 180 185 190

Leu Val Cys Gly Arg Ile Ser Leu Ala Lys Glu Val Phe Gly Glu Thr 195 200 205

Leu Asn Glu Ser Arg Asp Pro Asp Arg Ala Pro Glu Arg Tyr Thr Ser 210 215 220

Arg Phe Tyr Leu Lys Phe Lys His Leu Glu Arg Ala Phe Asp Met Leu 225 230 235 240

Ser Glu Cys Gly Phe His Met Val Ala Cys Asn Ser Ser Val Thr Ala 245 250 255

Ser	Phe	Ile	Asn 260	Gln	Tyr	Thr	Asp	Asp 265	Lys	Ile	Trp	Ser	270	Tyr	Tnr		
Glu	Tyr	Val 275	Phe	Tyr	Arg	Glu	Pro 280	Ser	Arg	Trp	Ser	Pro 285	Ser	His	Cys		
Asp	Cys 290	Cys	Cys	Lys	Asn	Gly 295	Lys	Gly	Asp	Lys	Glu 300	Gly	Glu	Ser	Gly		
Thr 305	Ser	Cys	Asn	Asp	Leu 310	Ser	Thr	Ser	Ser	Cys 315	Asp	Ser	Gln	Ser	Glu 320		
Ala	Ser	Ser	Pro	Gln 325	Glu	Thr	Val	Ile	Cys 330	Gly	Pro	Val	Thr	Arg 335	Gln		
Thr	Asn	Ile	Gln 340	Thr	Leu	Asp	Arg	Pro 345	Ile	Lys	Lys	Gly	Pro 350	Val	Gln		
Leu	Ile	Gln 355		Ser	Glu	Met	Arg 360		Lys	Ser	Asp	Leu 365	Leu	Arg	Ile		
Leu	Thr 370		Gly	Ser	Arg	Glu 375		Asn	Met	Ser	Ser 380		Lys	Lys	Ala		
Val 385	_	Glu	Lys	Leu	Ser 390	Ile	Glu	Glu	Glu	Leu 395		Lys	Cys	Ile	Gln 400		
Asp	Phe	Leu	. Lys	Lys 405		Ile	Pro	Asp	Arg 410		Pro	Glu	ı Arg	Lys 415	His		
Pro	Trp	Gln	Ser 420		. Leu	Leu	. Arg	Lys 425		His	Leu	i					
<21	1>	3 769 DNA Homo	sap	oiens	3												
<40 agg	0> tcat	3 :ttt	ttaa	itaac	gtt a	ıgcat	cctt	it to	cctt	tctt	aca	agtt	gat	ccaa	aggata		60
															ıaaggga	1	20
caa	ıtggo	ctct	gagt	ggaa	aac t	gtag	gtcgt	t at	tato	cctcc	g aga	aacaa	aggg	tccç	gcagttc	1	180
CC	acto	actt	ccct	gagg	ata c	rtaga	acto	ra at	atco	aaaa	g tca	aagtt	tat	ttta	actcgcc	2	240

attccacatt	gataagcatc	cctcattccc	tcctgtggaa	aatgttttcc	ccaaagagag	300
acacggctaa	tgatctagcc	aaggactcca	agggaaggtt	tttcattgac	agagatggat	360
tcttgttccg	ttatattctg	gactatctca	gggacaggca	ggtggtcctg	cctgatcact	420
ttccagaaaa	aggaagactg	aaaagggaag	ctgaatactt	ccagctccca	gacttggtca	480
aactcctgac	ccccgatgaa	atcaagcaaa	gcccagatga	attctgccac	agtgactttg	540
aagatgcctc	ccaaggaagc	gacacaagaa	tetgeecec	ttcctccctg	ctccctgccg	600
accgcaagtg	gggtttcatt	actgtgggtt	acagaggatc	ctgcaccttg	ggcagagagg	660
gacaggcaga	tgccaagttt	cggagagttc	cccggatttt	ggtttgtgga	aggatttcct	720
tggcaaaaga	agtctttgga	gaaactttga	atgaaagcag	agaccctga		769
<210> 4						

<211> 237 <212> PRT <213> Homo sapiens

<400> 4

Met Asp Asn Gly Asp Trp Gly Tyr Met Met Thr Asp Pro Val Thr Leu

Asn Val Gly Gly His Leu Tyr Thr Thr Ser Leu Thr Thr Leu Thr Arg 25

Tyr Pro Asp Ser Met Leu Gly Ala Met Phe Gly Gly Asp Phe Pro Thr

Ala Arg Asp Pro Gln Gly Asn Tyr Phe Ile Asp Arg Asp Gly Pro Leu

Phe Arg Tyr Val Leu Asn Phe Leu Arg Thr Ser Glu Leu Thr Leu Pro

Leu Asp Phe Lys Glu Phe Asp Leu Leu Arg Lys Glu Ala Asp Phe Tyr 90

Gln Ile Glu Pro Leu Ile Gln Cys Leu Asn Asp Pro Lys Pro Leu Tyr

Pro Met Asp Thr Phe Glu Glu Val Val Glu Leu Ser Ser Thr Arg Lys 120

Leu Ser Lys Tyr Ser Asn Pro Val Ala Val Ile Ile Thr Gln Leu Thr 130

Ile Thr Thr Lys Val His Ser Leu Leu Glu Gly Ile Ser Asn Tyr Phe 150 155 145

Thr Lys Trp Asn Lys His Met Met Asp Thr Arg Asp Cys Gln Val Ser 165 170 175

Phe Thr Phe Gly Pro Cys Asp Tyr His Gln Glu Val Ser Leu Arg Val 180 185 190

His Leu Met Glu Tyr Ile Thr Lys Gln Gly Phe Thr Ile Arg Asn Thr 195 200 205

Arg Val His His Met Ser Glu Arg Ala Asn Glu Asn Thr Val Glu His 210 215 220

Asn Trp Thr Phe Cys Arg Leu Ala Arg Lys Thr Asp Asp 225 230 235

<210> 5

<211> 228

<212> PRT

<213> Drosophila melanogaster

<400> 5

Met Pro Glu Ile Ile Glu Leu Asn Val Gly Gly Val Ser Tyr Thr Thr 1 5 10 15

Thr Leu Ala Thr Leu Leu Gln Asp Lys Ser Thr Leu Leu Ala Glu Leu 20 25 30

Phe Gly Glu Gly Arg Asp Ser Leu Ala Lys Asp Ser Lys Gly Arg Tyr 35 40 . 45

Phe Leu Asp Arg Asp Gly Val Leu Phe Arg Tyr Ile Leu Asp Phe Leu 50 55 60

Arg Asp Lys Ala Leu His Leu Pro Glu Gly Phe Arg Glu Arg Gln Arg 65 70 75 80

Leu Leu Arg Glu Ala Glu His Phe Lys Leu Thr Ala Met Leu Glu Cys 85 90 95

Ile Arg Ser Glu Arg Asp Ala Arg Pro Pro Gly Cys Ile Thr Ile Gly 100 105 110

Tyr Arg Gly Ser Phe Gln Phe Gly Lys Asp Gly Leu Ala Asp Val Lys 115 120 125

Phe Arg Lys Leu Ser Arg Ile Leu Val Cys Gly Arg Val Ala Gln Cys 130 135 140

Arg Glu Val Phe Gly Asp Thr Leu Asn Glu Ser Arg Asp Pro Asp His 145 150 155 160

Gly Gly Thr Asp Arg Tyr Thr Ser Arg Phe Phe Leu Lys His Cys Tyr 165 170 175

Ile Glu Gln Ala Phe Asp Asn Leu His Asp His Gly Tyr Arg Met Ala 180 185 190

```
Gly Ser Cys Gly Ser Gly Thr Ala Gly Ser Ala Ala Glu Pro Lys Pro
Gly Val Asp Thr Glu Glu Asn Arg Trp Asn His Tyr Asn Glu Phe Val
                       215
Phe Ile Arg Asp
225
<210> 6
      190
<211>
      PRT
<212>
<213> Caenorhabditis elegans
<400> 6
Met Thr Ser Val Glu Asp Val Ile Thr Leu Asn Val Gly Gly Thr Met
Tyr Thr Thr Thr Arg Ser Thr Leu Ser Lys Glu Thr Asp Thr Leu Leu
Ala Asn Ile Ala Ser Gly Ser Leu Ser Glu Asp Glu Gln Ala Asn Val
Val Thr Leu Pro Asp Gly Thr Leu Phe Val Asp Arg Asp Gly Pro Leu
                        55
Phe Ala Tyr Val Leu His Phe Leu Arg Thr Asp Lys Leu Ser Leu Pro
                    70
Glu Gln Phe Arg Glu Val Ala Arg Leu Lys Asp Glu Ala Asp Phe Tyr
Arg Leu Glu Arg Phe Ser Thr Leu Leu Ser Asn Ala Ser Ser Ile Ser
            100
Pro Arg Pro Arg Thr Ala Asn Gly Tyr Asn Thr Ile Thr Ser Gly Ala
                            120
Glu Thr Gly Gly Tyr Ile Thr Leu Gly Tyr Arg Gly Thr Phe Ala Phe
Gly Arg Asp Gly Gln Ala Asp Val Lys Phe Arg Lys Leu His Arg Ile
                    150
                                        155
Leu Val Cys Gly Arg Ala Thr Leu Cys Arg Glu Val Phe Ala Asp Thr
               165
Leu Asn Glu Ser Arg Asp Pro Gly Gly Pro Asp Asp Gly Glu
                                185
```

<210> 7

<211> 256

<212> PRT

<213> Homo sapiens

```
<220>
```

<223> wherein "Xaa" is unknown.

<400> 7

Met Ser Arg Pro Leu Ile Thr Arg Ser Pro Ala Ser Pro Leu Xaa Asn 1 5 10 15

Gln Gly Ile Pro Thr Pro Ala Gln Leu Thr Lys Ser Asn Ala Pro Val 20 25 30

His Ile Asp Val Gly Gly His Met Tyr Thr Ser Ser Leu Ala Thr Leu 35 40 45

Thr Lys Tyr Pro Glu Ser Arg Ile Gly Arg Leu Phe Asp Gly Thr Glu 50 55 60

Pro Ile Val Leu Asp Ser Leu Lys Gln His Tyr Phe Ile Asp Arg Asp 65 70 75 80

Gly Gln Met Phe Arg Tyr Ile Leu Asn Phe Leu Arg Thr Ser Lys Leu 85 90 95

Leu Ile Pro Asp Asp Phe Lys Asp Tyr Thr Leu Leu Tyr Glu Glu Ala 100 105 110

Lys Tyr Phe Gln Leu Gln Pro Met Leu Leu Glu Met Glu Arg Trp Lys 115 120 125

Gln Asp Arg Glu Thr Gly Arg Phe Ser Arg Pro Cys Glu Cys Leu Val 130 135 140

Lys Ser Leu Ile Glu Glu Val Phe Pro Glu Ile Gly Asp Val Met Cys 165 170 175

Asn Ser Val Asn Ala Gly Trp Asn His Asp Ser Thr His Val Ile Arg 180 185 190

Phe Pro Leu Asn Gly Tyr Cys His Leu Asn Ser Val Gln Val Leu Glu 195 200 205

Arg Leu Gln Gln Arg Gly Phe Glu Ile Val Gly Ser Cys Gly Gly Gly 210 215 220

Val Asp Ser Ser Gln Phe Ser Glu Tyr Val Leu Arg Arg Glu Leu Arg 225 230 235 240

Arg Thr Pro Arg Val Pro Ser Val Ile Arg Ile Lys Gln Glu Pro Leu 245 250 255

<221> variant

<222> (15)..(15)

<213> Homo sapiens

```
<210> 8
<211> 80
<212> DNA
<213> Artificial
<220>
<223> Synthetic Oligonucleotide Modified To Contain Biotin at the 5 Pr
       ime En
<400>
      8
tgggagctgg aagtattcag cttccctttt cagtcttcct ttttctggaa agtgatcagg
                                                                      60
                                                                      80
caggaccacc tgcctgtccc
<210> 9
<211> 20
<212> DNA
<213> Homo sapiens
<400> 9
tactcgccat tccacattga
                                                                      20
<210> 10
<211> 20
<212> DNA
<213> Homo sapiens
<400> 10
attcatctgg gctttgcttg
                                                                      20
<210> 11
<211> 14
<212> PRT
<213> Homo sapiens
<400> 11
Met Ala Leu Ser Gly Asn Cys Ser Arg Tyr Tyr Pro Arg Glu
                                   10
<210> 12
<211> 14
<212> PRT
<213> Homo sapiens
<400> 12
Phe Gly Glu Thr Leu Asn Glu Ser Arg Asp Pro Asp Arg Ala
<210> 13
<211> 14
<212> PRT
```

```
<400> 13
His Met Val Ala Cys Asn Ser Ser Val Thr Ala Ser Phe Ile
                                  10
<210> 14
<211> 14
<212> PRT
<213> Homo sapiens
<400> 14
Gly Ser Arg Glu Ser Asn Met Ser Ser Lys Lys Ala Val
              5
<210> 15
<211> 13
<212> PRT
<213> Homo sapiens
<400> 15
Leu Trp Lys Met Phe Ser Pro Lys Arg Asp Thr Ala Asn
               5
<210> 16
<211> 13
<212> PRT
<213> Homo sapiens
<400> 16
Ala Pro Glu Arg Tyr Thr Ser Arg Phe Tyr Leu Lys Phe
                5
<210> 17
<211> 13
<212> PRT
<213> Homo sapiens
<400> 17
Arg Glu Ser Asn Met Ser Ser Lys Lys Ala Val Lys
                5
<210> 18
<211> 13
 <212> PRT
 <213> Homo sapiens
 <400> 18
 Glu Ser Asn Met Ser Ser Lys Lys Lys Ala Val Lys Glu
                5
 <210> 19
```

```
<211> 18
      PRT
<212>
<213> Homo sapiens
<400> 19
Phe Pro Glu Lys Gly Arg Leu Lys Arg Glu Ala Glu Tyr Phe Gln Leu
Pro Asp
<210> 20
<211> 103
<212> PRT
<213> Homo sapiens
<400> 20
Glu Val Val Glu Leu Asn Val Gly Gly Gln Val Tyr Phe Thr Arg His
Ser Thr Leu Ile Ser Ile Pro His Ser Leu Leu Trp Lys Met Phe Ser
                                25
Pro Lys Arg Asp Thr Ala Asn Asp Leu Ala Lys Asp Ser Lys Gly Arg
Phe Phe Ile Asp Arg Asp Gly Phe Leu Phe Arg Tyr Ile Leu Asp Tyr
                        55
Leu Arg Asp Arg Gln Val Val Leu Pro Asp His Phe Pro Glu Lys Gly
Arg Leu Lys Arg Glu Ala Glu Tyr Phe Gln Leu Pro Asp Leu Val Lys
                                    90
Leu Leu Thr Pro Asp Glu Ile
            100
<210> 21
<211> 21
 <212> PRT
 <213> Homo sapiens
 <400> 21
Cys Gly Phe His Met Val Ala Cys Asn Ser Ser Val Thr Ala Ser Phe
 Ile Asn Gln Tyr Thr
             20
 <210> 22
 <211> 17
 <212> DNA
 <213> Homo sapiens
```

tgggattcgg gctt	tgg				17
<210> 23 <211> 26 <212> DNA <213> Homo sap	piens				
<400> 23 tgttgggttg ttac	cagacat cataaa				26
<210> 24 <211> 29 <212> DNA <213> Homo sap	piens				
<400> 24 tgacacagct aaat	cectage atgggeaca				29
<210> 25 <211> 733 <212> DNA <213> homo sap	oiens				
<400> 25 gggateegga geed	caaatct tctgacaaa	a ctcacacatg	cccaccgtgc	ccagcacctg	60
aattegaggg tgea	accgtca gtcttcctc	t tccccccaaa	acccaaggac	accctcatga	120
teteceggae teet	gaggtc acatgegtg	g tggtggacgt	aagccacgaa	gaccctgagg	180
tcaagttcaa ctgc	gtacgtg gacggcgtg	g aggtgcataa	tgccaagaca	aagccgcggg	240
aggagcagta caac	cagcacg taccgtgtg	g tcagcgtcct	caccgtcctg	caccaggact	300
ggctgaatgg caag	ggagtac aagtgcaag	g tctccaacaa	agccctccca	acccccatcg	360
agaaaaccat ctcc	caaagcc aaagggcag	c cccgagaacc	acaggtgtac	accctgcccc	420
cateceggga tgag	jctgacc aagaaccag	g tcagcctgac	ctgcctggtc	aaaggcttct	480
atccaagcga catc	egcegtg gagtgggag	a gcaatgggca	gccggagaac	aactacaaga	540
ccacgcctcc cgtg	getggae teegaegge	t ccttcttcct	ctacagcaag	ctcaccgtgg	600
acaagagcag gtgg	gcagcag gggaacgtc	t tctcatgctc	cgtgatgcat	gaggetetge	660
acaaccacta cacg	gcagaag agcctctcc	c tgtctccggg	taaatgagtg	cgacggccgc	720
gactctagag gat					733

<210> 26

<211> <212>		
<213>	bacteriophage T7	
<400>	26	
Asp Ty 1	r Lys Asp Asp Asp Lys 5	
<210> <211> <212> <213>		
<400> gcagca	27 gegg eegeeetgag gtggtagage tgaatgteg	39
<210> <211> <212> <213>	28 36 DNA Homo sapiens	
<400> gcagca	28 gtcg actagatgat acttccttaa aagttc	36
<210> <211> <212> <213>		
<400> gcagca	29 gcgg ccgcatggct ctgagtggaa actgtagtc	39
<210> <211> <212> <213>	30 37 DNA Homo sapiens	
<400> gcagca	30 gtcg actgtatatt ggttgatgaa agatgct	37
<210> <211> <212> <213>	23 DNA	
<400> caggtg	31 cagc tggtgcagte tgg	23
<210> <211> <212>	32 23 DNA	

<213> Homo sapiens	
<400> 32 caggtcaact taagggagtc tgg	23
<210> 33 <211> 23 <212> DNA <213> Homo sapiens	
<400> 33 gaggtgcagc tggtggagtc tgg	23
<210> 34 <211> 23 <212> DNA <213> Homo sapiens	
<400> 34 caggtgcagc tgcaggagtc ggg	23
<210> 35 <211> 23 <212> DNA <213> Homo sapiens <400> 35 gaggtgcagc tgttgcagtc tgc	23
<210> 36 <211> 23 <212> DNA <213> Homo sapiens	
<400> 36 caggtacagc tgcagcagtc agg	23
<210> 37 <211> 24 <212> DNA <213> Homo sapiens	
<400> 37 tgaggagacg gtgaccaggg tgcc	24
<210> 38 <211> 24 <212> DNA <213> Homo sapiens	-
<400> 38	

tgaagagacg gtgaccattg tccc	24
<210> 39 <211> 24 <212> DNA <213> Homo sapiens	
<400> 39 tgaggagacg gtgaccaggg ttcc	24
<210> 40 <211> 24 <212> DNA <213> Homo sapiens	
<400> 40 tgaggagacg gtgaccgtgg tccc	24
<210> 41 <211> 23 <212> DNA <213> Homo sapiens	
<400> 41 gacatccaga tgacccagtc tcc	23
<210> 42 <211> 23 <212> DNA <213> Homo sapiens	
<400> 42 gatgttgtga tgactcagtc tcc	23
<210> 43 <211> 23 <212> DNA <213> Homo sapiens	
<400> 43 gatattgtga tgactcagtc tcc	23
<210> 44 <211> 23 <212> DNA	
<213> Homo sapiens <400> 44 gaaattgtgt tgacgcagtc tcc	23

<210> <211> <212> <213>	45 23 DNA Homo sapiens	
	45 gtga tgacccagtc tcc	23
<210> <211> <212> <213>	DNA	
<400> gaaacg	46 racac tcacgcagtc tcc	23
<210> <211> <212>	23	
<213> <400>	Homo sapiens 47	23
gaaatt	Egtge tgactcagte tee	
<210> <211> <212> <213>	DNA	
<400> cagtc	48 tgtgt tgacgcagcc gcc	23
<210><211><212><213>	23 DNA	
<400>		23
<210> <211> <212>	DNA	
<213>	Homo sapiens	
<400> tccta	> 50 atgtge tgaeteagee ace	23
<210 <211 <212	> 23	

<213> Homo sapiens	
<400> 51 tcttctgagc tgactcagga ccc	23
<210> 52 <211> 23 <212> DNA <213> Homo sapiens	
<400> 52 cacgttatac tgactcaacc gcc	23
<210> 53 <211> 23 <212> DNA <213> Homo sapiens	
<400> 53 caggetgtge teacteagee gte	23
<210> 54 <211> 23 <212> DNA <213> Homo sapiens <400> 54 aattttatgc tgactcagcc cca	23
<210> 55 <211> 24 <212> DNA <213> Homo sapiens	
<400> 55 acgtttgatt tecacettgg tece	24
<210> 56 <211> 24 <212> DNA <213> Homo sapiens	
<400> 56 acgtttgatc tccagcttgg tccc	24
<210> 57 <211> 24 <212> DNA <213> Homo sapiens	
<400> 57	

acgtttgata tccactttgg tccc	24
<210> 58 <211> 24 <212> DNA <213> Homo sapiens	
<400> 58 acgtttgatc tccaccttgg tccc	24
<210> 59 <211> 24 <212> DNA <213> Homo sapiens	
<400> 59 acgtttaatc tccagtcgtg tccc	24
<210> 60 <211> 23 <212> DNA <213> Homo sapiens	
<400> 60 cagtctgtgt tgacgcagcc gcc	23
<210> 61 <211> 23 <212> DNA <213> Homo sapiens	
<400> 61 cagtetgeec tgaeteagee tge	23
<210> 62 <211> 23 <212> DNA <213> Homo sapiens	
<400> 62 tectatgtge tgaeteagee ace	23
<210> 63 <211> 23 <212> DNA <213> Homo sapiens	
<400> 63 tettetgage tgaeteagga eec	23

<210 <211 <212 <213	.> 2 ?> [54 23 DNA Homo	sapi	ens												
<400 cacg		54 cac t	gact	caad	ec go	cc										23
<400	.> 2 ?> I ?> I	ONA Homo	sapi		cc gt	.c										23
	.> 2 ?> I	23 DNA	sapi	Lens												
<400 aatt		66 Egc t	cgact	cago	cc c(ca										23
<210 <211 <212 <213	2> 3 2> F	67 301 PRT Drosc	ophil	la me	eland	ogast	ier									
<400)> (67														
Met 1	Ser	Glu	Ser	Met 5	Ser	Gly	Asp	His	Lys 10	Ile	Leu	Leu	Lys	Gly 15	His	
Ser	Ser	Gln	Tyr 20	Leu	Lys	Leu	Asn	Val 25	Gly	Gly	His	Leu	Tyr 30	Tyr	Thr	
Thr	Ile	Gly 35	Thr	Leu	Thr	Lys	Asn 40	Asn	Asp	Thr	Met	Leu 45	Ser	Ala	Met	
Phe	Ser 50	Gly	Arg	Met	Glu	Val 55	Leu	Thr	Asp	Ser	Glu 60	Gly	Trp	Ile	Leu	
Ile 65	Asp	Arg	Cys	Gly	Asn 70	His	Phe	Gly	Ile	Ile 75	Leu	Asn	Tyr	Leu	Arg 80	
Asp	Gly	Thr	Val	Pro 85	Leu	Pro	Glu	Thr	Asn 90	Lys	Glu	Ile	Ala	Glu 95	Leu	
Leu	Ala	Glu	Ala 100	Lys	Tyr	Tyr	Cys	Ile 105	Thr	Glu	Leu	Ala	Ile 110	Ser	Cys	
Glu	Arg	Ala 115	Leu	Tyr	Ala	His	Gln 120	Glu	Pro	Lys	Pro	Ile 125	Cys	Arg	Ile	

Pro	Leu 130	Ile	Thr	Ser	Gln	Lys 135	Glu	Glu	Gln	Leu	Leu 140	Leu	Ser	Val	Ser	
Leu 145	Lys	Pro	Ala	Val	Ile 150	Leu	Val	Val	Gln	Arg 155	Gln	Asn	Asn	Lys	Tyr 160	
Ser	Tyr	Thr	Ser	Thr 165	Ser	Asp	Asp	Asn	Leu 170	Leu	Lys	Asn	Ile	Glu 175	Leu	
Phe	Asp	Lys	Leu 180	Ser	Leu	Arg	Phe	Asn 185	Glu	Arg	Ile	Leu	Phe 190	Ile	Lys	
Asp	Val	Ile 195	Gly	Pro	Ser	Glu	Ile 200	Cys	Cys	Trp	Ser	Phe 205	Tyr	Gly	His	
Gly	Lys 210	Lys	Val	Ala	Glu	Val 215	Cys	Cys	Thr	Ser	Ile 220	Val	Tyr	Ala	Thr	
Asp 225	Arg	Lys	His	Thr	Lys 230	Val	Glu	Phe	Pro	Glu 235	Ala	Arg	Ile	Tyr	Glu 240	
Glu	Thr	Leu	Gln	Val 245	Leu	Leu	Tyr	Glu	Asn 250	Arg	Asn	Ala	Pro	Asp 255	Gln	
Glu	Leu	Met	Gln 260	Ala	Thr	Ser	Ser	Ala 265	Arg	Val	Gly	Ser	Ala 270	Ser	Gly	
Thr	Ser	Ile 275	Asn	Gln	Tyr	Thr	Ser 280	Asp	Glu	Glu	Glu	Glu 285	Arg	Thr	Gly	
Leu	Ala 290	Arg	Leu	Arg	Ser	Asn 295	Lys	Arg	Asn	Asn	Pro 300	Ser				
<210 <211 <212	1> 2	68 20 DNA														
<213			phil	la me	eland	ogast	er									
<400 atga		68 Etg (gatca	agctt	t											20
<210 <211	1> 2	69 20														
<212 <213		ONA Oroso	phil	La me	elano	ogast	cer									
<400 cct		69 cct (gacat	tcca	at											20
<210 <211 <212	L> 2 2> I	70 21 DNA														
<213	3> [Oroso	phil	La me	elano	ogast	cer									

<pre><400> 70 actgcagccg attcattaat g</pre>	21
<210> 71 <211> 48 <212> DNA <213> Drosophila melanogaster	
<400> 71 gaattaatac gactcactat agggagatat catacacata cgatttag	48
<210> 72 <211> 48 <212> DNA <213> Drosophila melanogaster	
<400> 72 gaattaatac gactcactat agggagacat gattacgcca agctcgaa	48
<210> 73 <211> 21 <212> DNA <213> Drosophila melanogaster	
<400> 73 tgtaaaacga cggccagtga a	21